



#21

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/518763
Source: AU 1636
Date Processed by STIC: 10/01/01

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NOV 13 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/518 763</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY FTO		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <220>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
13 <input type="checkbox"/> Misuse of n	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
		It can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/518,763

DATE: 10/01/2001
TIME: 09:47:31

Input Set : A:\PTO.txt
Output Set: N:\CRF3\10012001\I518763.raw

3 <110> APPLICANT: Boyce Thompson Institute for Plant Research
4 Blissard, Gary
5 Robert, Granados
6 Guangyun, Lin
8 <120> TITLE OF INVENTION: STABLE CELL LINES RESISTANT TO APOPTOSIS AND NUTRIENT STRESS
AND METHODS

9 OF MAKING SAME

11 <130> FILE REFERENCE: BTI-44

13 <140> CURRENT APPLICATION NUMBER: US 09/518,763

14 <141> CURRENT FILING DATE: 2000-03-03

16 <160> NUMBER OF SEQ ID NOS: 11

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 900

22 <212> TYPE: DNA

23 <213> ORGANISM: Autographa californica nucleopolyhedrovirus *See page 2
and Error Summary Sheet
Item 10*

25 <400> SEQUENCE: 1

26 atgtgtgtaa	tttttccgtt	agaaaatcgac	gtgtcccaga	cgattattcg	agattgtcag	60
28 gtggacaaac	aaaccagaga	gttgggtgtac	attaacaaga	ttatgaacac	gcaattgaca	120
30 aaacccgttc	tcatgatgtt	taacatttcg	ggtcctatac	gaagcgttac	gchgcaagaac	180
32 aacaatttgc	gcgacagaat	aaaatcaaaa	gtcgatgaac	aatttgcata	actagaacgc	240
34 gattacagcg	atcaaatttgc	tggattccac	gatagcatca	agtattttaa	agatgaacac	300
36 tattcggtaa	gttgcacaaa	tggcagcgtg	ttgaaaagca	agtttgcataa	aattttaaag	360
38 agtcatgatt	ataccgataa	aaagtctatt	gaagcttacg	agaaataactg	tttgcacaaa	420
40 ttggcgtacg	aacgcaacga	ctactacgtg	gcccgtatgcg	ttgtgaagcc	gggatttgag	480
42 aacggcagca	accaagtgc	atctttcgag	tacaacccga	ttggtaacaa	agttattgtg	540
44 ccgtttgctc	acgaaattaa	cgacacggga	ctttacgagt	acgacgtcg	agcttacgtg	600
46 gacagtgtgc	agtttgcata	cgaaacaaattt	gaagagtttgc	tgcagagttt	aatattgccc	660
48 tcgtcggtca	aaaattcggaa	aaaggtttta	tattacaacg	aagcgtcggaa	aaacaaaagc	720
50 atgatctaca	aggctttaga	gtttactaca	gaatcgagct	ggggcaaaatc	cgaaaagttat	780
52 aattggaaaa	tttttgcataa	cggttttatt	tatgataaaaa	aatcaaaaagt	gttgcgtatgtt	840
54 aaattgcaca	atgtacttag	tgcactcaac	aaaaatgtaa	tattaaacac	aattaaataaa	900

57 <210> SEQ ID NO: 2

58 <211> LENGTH: 299

59 <212> TYPE: PRT

60 <213> ORGANISM: Autographa californica nucleopolyhedrovirus

62 <400> SEQUENCE: 2

64 Met Cys Val Ile Phe Pro Val Glu Ile Asp Val Ser Gln Thr Ile Ile						
65 1	5	10	15			
67 Arg Asp Cys Gln Val Asp Lys Gln Thr Arg Glu Leu Val Tyr Ile Asn						
68	20	25	30			
70 Lys Ile Met Asn Thr Gln Leu Thr Lys Pro Val Leu Met Met Phe Asn						
71	35	40	45			
73 Ile Ser Gly Pro Ile Arg Ser Val Thr Arg Lys Asn Asn Asn Leu Arg						
74	50	55	60			
76 Asp Arg Ile Lys Ser Lys Val Asp Glu Gln Phe Asp Gln Leu Glu Arg						
77 65	70	75	80			
79 Asp Tyr Ser Asp Gln Met Asp Gly Phe His Asp Ser Ile Lys Tyr Phe						

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Output Set: N:\CRF3\10012001\I518763.raw

```

80          85          90          95
82 Lys Asp Glu His Tyr Ser Val Ser Cys Gln Asn Gly Ser Val Leu Lys
83          100          105          110
85 Ser Lys Phe Ala Lys Ile Leu Lys Ser His Asp Tyr Thr Asp Lys Lys
86          115          120          125
88 Ser Ile Glu Ala Tyr Glu Lys Tyr Cys Leu Pro Lys Leu Val Asp Glu
89          130          135          140
91 Arg Asn Asp Tyr Tyr Val Ala Val Cys Val Leu Lys Pro Gly Phe Glu
92 145          150          155          160
94 Asn Gly Ser Asn Gln Val Leu Ser Phe Glu Tyr Asn Pro Ile Gly Asn
95          165          170          175
97 Lys Val Ile Val Pro Phe Ala His Glu Ile Asn Asp Thr Gly Leu Tyr
98          180          185          190
100 Glu Tyr Asp Val Val Ala Tyr Val Asp Ser Val Gln Phe Asp Gly Glu
101          195          200          205
103 Gln Phe Glu Glu Phe Val Gln Ser Leu Ile Leu Pro Ser Ser Phe Lys
104          210          215          220
106 Asn Ser Glu Lys Val Leu Tyr Tyr Asn Glu Ala Ser Lys Asn Lys Ser
107 225          230          235          240
109 Met Ile Tyr Lys Ala Leu Glu Phe Thr Thr Glu Ser Ser Trp Gly Lys
110          245          250          255
112 Ser Glu Lys Tyr Asn Trp Lys Ile Phe Cys Asn Gly Phe Ile Tyr Asp
113          260          265          270
115 Lys Lys Ser Lys Val Leu Tyr Val Lys Leu His Asn Val Thr Ser Ala
116          275          280          285
118 Leu Asn Lys Asn Val Ile Leu Asn Thr Ile Lys
119          290          295
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 38
123 <212> TYPE: DNA
124 <213> ORGANISM: synthetic construct
126 <400> SEQUENCE: 3
127 ctagaaggtt gaaagatgcc agcggctgtt cgtaatag
130 <210> SEQ ID NO: 4
131 <211> LENGTH: 38
132 <212> TYPE: DNA
133 <213> ORGANISM: synthetic construct
135 <400> SEQUENCE: 4
136 ctagcttata cgaccagccg ctggcatctt tccaaactt
139 <210> SEQ ID NO: 5
140 <211> LENGTH: 30
141 <212> TYPE: DNA
142 <213> ORGANISM: synthetic construct
144 <400> SEQUENCE: 5
145 cagaattcat gtgtgttaatt tttccggtag
148 <210> SEQ ID NO: 6
149 <211> LENGTH: 33
150 <212> TYPE: DNA
151 <213> ORGANISM: synthetic construct

```

Errored: Invalid 213 response.
Appropriate responses are "Artificial Sequence",
"Unknown" or the name of³⁸ some
specific species.

See Error Summary Sheet.

FYI: A 213 response of "Artificial Sequence" requires an explanation
for example "synthetic ~~construct~~³⁰ construct"
in field 223.

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PATENT APPLICATION: US/09/518,763

DATE: 10/01/2001
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Input Set : A:\PTO.txt
Output Set: N:\CRF3\10012001\I518763.raw

153 <400> SEQUENCE: 6	
154 ttttgctcta gatttaattg tgtttaatat tac	33
157 <210> SEQ ID NO: 7	
158 <211> LENGTH: 35	
159 <212> TYPE: DNA	
160 <213> ORGANISM: synthetic construct	
162 <400> SEQUENCE: 7	
163 aatgctctag attatattaat tgtgttaat attac	35
166 <210> SEQ ID NO: 8	
167 <211> LENGTH: 15	
168 <212> TYPE: DNA	
169 <213> ORGANISM: synthetic construct	
171 <400> SEQUENCE: 8	
172 ttaaacacaaa ttaaaa	15
175 <210> SEQ ID NO: 9	
176 <211> LENGTH: 5	
177 <212> TYPE: PRT	
178 <213> ORGANISM: synthetic construct	
180 <400> SEQUENCE: 9	
182 Leu Asn Thr Ile Lys	
183 1 5	
185 <210> SEQ ID NO: 10	
186 <211> LENGTH: 54	
187 <212> TYPE: DNA	
188 <213> ORGANISM: synthetic construct	
190 <400> SEQUENCE: 10	
191 ttaaacacaaa ttaaatctag aagttggaaa gatgccagcg gctggtcgta atag	54
194 <210> SEQ ID NO: 11	
195 <211> LENGTH: 16	
196 <212> TYPE: PRT	
197 <213> ORGANISM: synthetic construct	
199 <400> SEQUENCE: 11	
201 Leu Asn Thr Ile Lys Ser Arg Ser Trp Lys Asp Ala Ser Gly Trp Ser	
202 1 5 10 15	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/518,763

DATE: 10/01/2001
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